ABSTRACT

The present invention concerns methods and systems for analysis of drug resistance in HIV-1. More specifically, the invention provides methods for predicting drug resistance by correlating genotypic information with phenotypic profiles. The methods allow the identification of primary and secondary resistance-associated mutations for new and existing drugs and for calculating the contribution of mutations and combinations of mutations to resistance and hyper-susceptibility. The invention allows the design, optimization and assessment of the efficiency of a therapeutic regimen based upon the genotype of the disease affecting a patient

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